

#4158
9/4/02
PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,877

DATE: 07/24/2001

TIME: 13:32:01

Input Set : A:\10179.204-US(sequence).ST25.txt

Output Set: N:\CRF3\07242001\I869877.raw

3 <110> APPLICANT: Schneider, Palle
4 Danielsen, Steffen
5 Svendsen, Allan
7 <120> TITLE OF INVENTION: Laccase Mutants
9 <130> FILE REFERENCE: 10179.204-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/869,877
C--> 11 <141> CURRENT FILING DATE: 2001-07-06
11 <160> NUMBER OF SEQ ID NOS: 10
13 <170> SOFTWARE: PatentIn version 3.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 539
17 <212> TYPE: PRT
18 <213> ORGANISM: Coprinus cinereus
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23 1 5 10 15
26 Asn Ala Gln Ile Val Asn Ser Val Asp Thr Met Thr Leu Thr Asn Ala
27 20 25 30
30 Asn Val Ser Pro Asp Gly Phe Thr Arg Ala Gly Ile Leu Val Asn Gly
31 35 40 45
34 Val His Gly Pro Leu Ile Arg Gly Gly Lys Asn Asp Asn Phe Glu Leu
35 50 55 60
38 Asn Val Val Asn Asp Leu Asp Asn Pro Thr Met Leu Arg Pro Thr Ser
39 65 70 75 80
42 Ile His Trp His Gly Leu Phe Gln Arg Gly Thr Asn Trp Ala Asp Gly
43 85 90 95
46 Ala Asp Gly Val Asn Gln Cys Pro Ile Ser Pro Gly His Ala Phe Leu
47 100 105 110
50 Tyr Lys Phe Thr Pro Ala Gly His Ala Gly Thr Phe Trp Tyr His Ser
51 115 120 125
54 His Phe Gly Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Met Val Ile
55 130 135 140
58 Tyr Asp Asp Asn Asp Pro His Ala Ala Leu Tyr Asp Glu Asp Asp Glu
59 145 150 155 160
62 Asn Thr Ile Ile Thr Leu Ala Asp Trp Tyr His Ile Pro Ala Pro Ser
63 165 170 175
66 Ile Gln Gly Ala Ala Gln Pro Asp Ala Thr Leu Ile Asn Gly Lys Gly
67 180 185 190
70 Arg Tyr Val Gly Gly Pro Ala Ala Glu Leu Ser Ile Val Asn Val Glu
71 195 200 205
74 Gln Gly Lys Lys Tyr Arg Met Arg Leu Ile Ser Leu Ser Cys Asp Pro
75 210 215 220
78 Asn Trp Gln Phe Ser Ile Asp Gly His Glu Leu Thr Ile Ile Glu Val
79 225 230 235 240
82 Asp Gly Gln Leu Thr Glu Pro His Thr Val Asp Arg Leu Gln Ile Phe
83 245 250 255
86 Thr Gly Gln Arg Tyr Ser Phe Val Leu Asp Ala Asn Gln Pro Val Asp

ENTERED

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87          260          265          270
90 Asn Tyr Trp Ile Arg Ala Gln Pro Asn Lys Gly Arg Asn Gly Leu Ala
91          275          280          285
94 Gly Thr Phe Ala Asn Gly Val Asn Ser Ala Ile Leu Arg Tyr Ala Gly
95          290          295          300
98 Ala Ala Asn Ala Asp Pro Thr Thr Ser Ala Asn Pro Asn Pro Ala Gln
99 305          310          315          320
102 Leu Asn Glu Ala Asp Leu His Ala Leu Ile Asp Pro Ala Ala Pro Gly
103          325          330          335
106 Ile Pro Thr Pro Gly Ala Ala Asp Val Asn Leu Arg Phe Gln Leu Gly
107          340          345          350
110 Phe Ser Gly Gly Arg Phe Thr Ile Asn Gly Thr Ala Tyr Glu Ser Pro
111          355          360          365
114 Ser Val Pro Thr Leu Leu Gln Ile Met Ser Gly Ala Gln Ser Ala Asn
115          370          375          380
118 Asp Leu Leu Pro Ala Gly Ser Val Tyr Glu Leu Pro Arg Asn Gln Val
119 385          390          395          400
122 Val Glu Leu Val Val Pro Ala Gly Val Leu Gly Gly Pro His Pro Phe
123          405          410          415
126 His Leu His Gly His Ala Phe Ser Val Val Arg Ser Ala Gly Ser Ser
127          420          425          430
130 Thr Tyr Asn Phe Val Asn Pro Val Lys Arg Asp Val Val Ser Leu Gly
131          435          440          445
134 Val Thr Gly Asp Glu Val Thr Ile Arg Phe Val Thr Asp Asn Pro Gly
135          450          455          460
138 Pro Trp Phe Phe His Cys His Ile Glu Phe His Leu Met Asn Gly Leu
139 465          470          475          480
142 Ala Ile Val Phe Ala Glu Asp Met Ala Asn Thr Val Asp Ala Asn Asn
143          485          490          495
146 Pro Pro Val Glu Trp Ala Gln Leu Cys Glu Ile Tyr Asp Asp Leu Pro
147          500          505          510
150 Pro Glu Ala Thr Ser Ile Gln Thr Val Val Arg Arg Ala Glu Pro Thr
151          515          520          525
154 Gly Phe Ser Ala Lys Phe Arg Arg Glu Gly Leu
155          530          535
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 499
160 <212> TYPE: PRT
161 <213> ORGANISM: Polyporus pinsitus
163 <400> SEQUENCE: 2
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166 1          5          10          15
169 Pro Asp Gly Phe Ser Arg Gln Ala Val Val Val Asn Gly Gly Thr Pro
170          20          25          30
173 Gly Pro Leu Ile Thr Gly Asn Met Gly Asp Arg Phe Gln Leu Asn Val
174          35          40          45
177 Ile Asp Asn Leu Thr Asn His Thr Met Leu Lys Ser Thr Ser Ile His
178          50          55          60
181 Trp His Gly Phe Phe Gln Lys Gly Thr Asn Trp Ala Asp Gly Pro Ala

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182	65					70					75				80	
185	Phe	Ile	Asn	Gln	Cys	Pro	Ile	Ser	Ser	Gly	His	Ser	Phe	Leu	Tyr	Asp
186					85					90					95	
189	Phe	Gln	Val	Pro	Asp	Gln	Ala	Gly	Thr	Phe	Trp	Tyr	His	Ser	His	Leu
190				100					105					110		
193	Ser	Thr	Gln	Tyr	Cys	Asp	Gly	Leu	Arg	Gly	Pro	Phe	Val	Val	Tyr	Asp
194			115					120					125			
197	Pro	Asn	Asp	Pro	Ala	Ala	Asp	Leu	Tyr	Asp	Val	Asp	Asn	Asp	Asp	Thr
198		130					135					140				
201	Val	Ile	Thr	Leu	Val	Asp	Trp	Tyr	His	Val	Ala	Ala	Lys	Leu	Gly	Pro
202	145					150					155				160	
205	Ala	Phe	Pro	Leu	Gly	Ala	Asp	Ala	Thr	Leu	Ile	Asn	Gly	Lys	Gly	Arg
206					165					170					175	
209	Ser	Pro	Ser	Thr	Thr	Thr	Ala	Asp	Leu	Ser	Val	Ile	Ser	Val	Thr	Pro
210				180					185					190		
213	Gly	Lys	Arg	Tyr	Arg	Phe	Arg	Leu	Val	Ser	Leu	Ser	Cys	Asp	Pro	Asn
214			195					200					205			
217	Tyr	Thr	Phe	Ser	Ile	Asp	Gly	His	Asn	Met	Thr	Ile	Ile	Glu	Thr	Asp
218		210					215					220				
221	Ser	Ile	Asn	Thr	Ala	Pro	Leu	Val	Val	Asp	Ser	Ile	Gln	Ile	Phe	Ala
222	225					230					235				240	
225	Ala	Gln	Arg	Tyr	Ser	Phe	Val	Leu	Glu	Ala	Asn	Gln	Ala	Val	Asp	Asn
226					245					250					255	
229	Tyr	Trp	Ile	Arg	Ala	Asn	Pro	Asn	Phe	Gly	Asn	Val	Gly	Phe	Thr	Gly
230				260					265					270		
233	Gly	Ile	Asn	Ser	Ala	Ile	Leu	Arg	Tyr	Asp	Gly	Ala	Ala	Ala	Val	Glu
234			275					280					285			
237	Pro	Thr	Thr	Thr	Gln	Thr	Thr	Ser	Thr	Ala	Pro	Leu	Asn	Glu	Val	Asn
238		290					295					300				
241	Leu	His	Pro	Leu	Val	Thr	Thr	Ala	Val	Pro	Gly	Ser	Pro	Val	Ala	Gly
242	305					310					315				320	
245	Gly	Val	Asp	Leu	Ala	Ile	Asn	Met	Ala	Phe	Asn	Phe	Asn	Gly	Thr	Asn
246					325					330					335	
249	Phe	Phe	Ile	Asn	Gly	Ala	Ser	Phe	Thr	Pro	Pro	Thr	Val	Pro	Val	Leu
250				340					345					350		
253	Leu	Gln	Ile	Ile	Ser	Gly	Ala	Gln	Asn	Ala	Gln	Asp	Leu	Leu	Pro	Ser
254			355					360					365			
257	Gly	Ser	Val	Tyr	Ser	Leu	Pro	Ser	Asn	Ala	Asp	Ile	Glu	Ile	Ser	Phe
258		370					375					380				
261	Pro	Ala	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Pro	His	Pro	Phe	His	Leu	His
262	385					390					395				400	
265	Gly	His	Ala	Phe	Ala	Val	Val	Arg	Ser	Ala	Gly	Ser	Thr	Val	Tyr	Asn
266					405					410					415	
269	Tyr	Asp	Asn	Pro	Ile	Phe	Arg	Asp	Val	Val	Ser	Thr	Gly	Thr	Pro	Ala
270				420					425					430		
273	Ala	Gly	Asp	Asn	Val	Thr	Ile	Arg	Phe	Arg	Thr	Asp	Asn	Pro	Gly	Pro
274			435					440					445			
277	Trp	Phe	Leu	His	Cys	His	Ile	Asp	Phe	His	Leu	Glu	Ala	Gly	Phe	Ala
278		450					455					460				

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281 Val Val Phe Ala Glu Asp Ile Pro Asp Val Ala Ser Ala Asn Pro Val
282 465                               470                               475                               480
285 Pro Gln Ala Trp Ser Asp Leu Cys Pro Thr Tyr Asp Ala Leu Asp Pro
286                               485                               490                               495
289 Ser Asp Gln
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 499
295 <212> TYPE: PRT
296 <213> ORGANISM: Polyporus pinsitus
298 <400> SEQUENCE: 3
300 Ala Ile Gly Pro Val Ala Ser Leu Val Val Ala Asn Ala Pro Val Ser
301 1                               5                               10                               15
304 Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro
305                               20                               25                               30
308 Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val
309                               35                               40                               45
312 Val Asp Thr Leu Thr Asn His Ser Met Leu Lys Ser Thr Ser Ile His
313                               50                               55                               60
316 Trp His Gly Phe Phe Gln Ala Gly Thr Asn Trp Ala Glu Gly Pro Ala
317 65                               70                               75                               80
320 Phe Val Asn Gln Cys Pro Ile Ala Ser Gly His Ser Phe Leu Tyr Asp
321                               85                               90                               95
324 Phe His Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu
325                               100                              105                              110
328 Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp
329                               115                              120                              125
332 Pro Lys Asp Pro His Ala Ser Arg Tyr Asp Val Asp Asn Glu Ser Thr
333                               130                              135                              140
336 Val Ile Thr Leu Thr Asp Trp Tyr His Thr Ala Ala Arg Leu Gly Pro
337 145                              150                              155                              160
340 Lys Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Leu Gly Arg
341                               165                              170                              175
344 Ser Ala Ser Thr Pro Thr Ala Ala Leu Ala Val Ile Asn Val Gln His
345                               180                              185                              190
348 Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser Ile Ser Cys Asp Pro Asn
349                               195                              200                              205
352 Tyr Thr Phe Ser Ile Asp Gly His Asn Leu Thr Val Ile Glu Val Asp
353                               210                              215                              220
356 Gly Ile Asn Ser Gln Pro Leu Leu Val Asp Ser Ile Gln Ile Phe Ala
357 225                              230                              235                              240
360 Ala Gln Arg Tyr Ser Phe Val Leu Asn Ala Asn Gln Thr Val Gly Asn
361                               245                              250                              255
364 Tyr Trp Val Arg Ala Asn Pro Asn Phe Gly Thr Val Gly Phe Ala Gly
365                               260                              265                              270
368 Gly Ile Asn Ser Ala Ile Leu Arg Tyr Gln Gly Ala Pro Val Ala Glu
369                               275                              280                              285
372 Pro Thr Thr Thr Gln Thr Pro Ser Val Ile Pro Leu Ile Glu Thr Asn
373                               290                              295                              300
376 Leu His Pro Leu Ala Arg Met Pro Val Pro Gly Ser Pro Thr Pro Gly

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```

377 305          310          315          320
380 Gly Val Asp Lys Ala Leu Asn Leu Ala Phe Asn Phe Asn Gly Thr Asn
381          325          330          335
384 Phe Phe Ile Asn Asn Ala Thr Phe Thr Pro Pro Thr Val Pro Val Leu
385          340          345          350
388 Leu Gln Ile Leu Ser Gly Ala Gln Thr Ala Gln Asp Leu Leu Pro Ala
389          355          360          365
392 Gly Ser Val Tyr Pro Leu Pro Ala His Ser Thr Ile Glu Ile Thr Leu
393          370          375          380
396 Pro Ala Thr Ala Leu Ala Pro Gly Ala Pro His Pro Phe His Leu His
397 385          390          395          400
400 Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Thr Tyr Asn
401          405          410          415
404 Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala
405          420          425          430
408 Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro
409          435          440          445
412 Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala
413          450          455          460
416 Ile Val Phe Ala Glu Asp Val Ala Asp Val Lys Ala Ala Asn Pro Val
417 465          470          475          480
420 Pro Lys Ala Trp Ser Asp Leu Cys Pro Ile Tyr Asp Gly Leu Ser Glu
421          485          490          495
424 Ala Asn Gln
428 <210> SEQ ID NO: 4
429 <211> LENGTH: 548
430 <212> TYPE: PRT
431 <213> ORGANISM: Phlebia radiata
433 <400> SEQUENCE:. 4
435 Met His Thr Phe Leu Arg Ser Thr Ala Leu Val Val Ala Gly Leu Ser
436 1          5          10          15
439 Ala Arg Ala Leu Ala Ser Ile Gly Pro Val Thr Asp Phe His Ile Val
440          20          25          30
443 Asn Ala Ala Val Ser Pro Asp Gly Phe Ser Arg Gln Ala Val Leu Ala
444          35          40          45
447 Glu Gly Val Phe Pro Gly Pro Leu Ile Ala Gly Asn Lys Gly Asp Asn
448          50          55          60
451 Phe Gln Ile Asn Val Ile Asp Glu Leu Thr Asn Ala Thr Met Leu Lys
452 65          70          75          80
455 Thr Thr Thr Ile His Trp His Gly Phe Phe Gln His Gly Thr Asn Trp
456          85          90          95
459 Ala Asp Gly Pro Ala Phe Ile Asn Gln Cys Pro Ile Ala Ser Gly Asp
460          100          105          110
463 Ser Phe Leu Tyr Asn Phe Gln Val Pro Asp Gln Ala Gly Thr Phe Trp
464          115          120          125
467 Tyr His Ser His Leu Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro
468          130          135          140
471 Phe Val Val Tyr Asp Pro Ala Asp Pro Tyr Leu Asp Gln Tyr Asp Val
472 145          150          155          160

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\10179.204-US(sequence).ST25.txt

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E:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:1260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9